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Result
No.
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Maximum
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: pir2:*
3: pir3:*
4: pir4:*
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class II INCENP pr
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ALIGNMENTS

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alpha-globulin B precursor (clone C72) - upland cotton N; Alternate names: seed storage protein; vicilin precursor C; Species: Gossypium hirsutum (upland cotton) C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_c) C; Accession: A30838; S06911 R; Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L. Plant Mol. Biol. 7, 475-489, 1986 A; Title: Developmental biochemistry of cottonseed embryoger A; Reference number: A30838
                                                                                                                                                                                                                    RESULT
FWCNAB
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C;Superfamily: glycinin
C;Keywords: seed; storage protein
F;1-24/Domain: signal sequence #status predi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X62625
A;Accession: S22478
A;Mclecule type: mRNA
A;Residues: 1-452 <MC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Theobroma cacao (cacao)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
C;Accession: S22477; S22478; S18105; S22050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _{\rm F;1-24/Domain}: signal sequence *status predicted F;25-566/Product: vicilin *status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-566 <MCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Comparison of the structure and nucleotide A;Reference number: S22477; MUID:92288309 A;Accession: S22477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; MCHenry, L.; Fritz, P.J. Plant Mol. Biol. 18, 1173-1176, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: X62626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vicilin precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 31.4
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                         95
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31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 172; DB
Pred. No. 2.6e
20; Mismatches
                                          of cottonseed embryogenesis and germination XVIII
                                                                                                                               30-Sep-1991 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
.6e-07;
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A; Residues: ...
C; Superfamilion
                  Plant
                                                                     C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
                                                                                                                alpha-globulin type A precursor - upland cotton
N;Alternate names: seed storage protein
                                                                                                                                                             RESULT
S06398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: Developmental blochemistry of cottonseed embryogenesis A;Reference number: S06398
A;Accession: S08059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: Gossypium hirsutum (upland cotton)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
C:Accession: S08059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-588 <CHL>
A;Cross references: GB:M16891; NID:g167374; PIDN:AAA33071.1; PID:g167375
A:Fxnerimental source: var. Coker 201
                                                                                                                                                                                                                                             Дb
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A; Residues: 1-81 <CH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: var. Coker 201
R;Chlan, C.A.; Borrotto, K.; Kamalay, J.A.; Dure III, L.
R;Chlan, Diol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis
                                      R; Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III,
                                                           C; Accession: S06398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-509 < CHL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Chlan, C.A.; Bo
Plant Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N; Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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A; Accession: S06911
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Comment: This is a seed storage protein; Superfamily: glycinin
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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                      Mol.
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  Developmental
                                                                                                                                                                                                                                             KKQQCVRECREKYQENPWRGEREEEAEEEE
                                                                                                                                                                                                                                                                                                                     DPQRRYEECQQEC---RQQEERQQPQCQQRCLKRFEQEQQQSQRQFQECQQHCHQQEQRPE 58
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                    Biol. 9,
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borroto, K.; Kamalay, J.A.; Dure III, 1. 9, 533-546, 1987
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                      533-546,
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biochemistry of
                                                                                                                                                                                                                                                                                                                                                                                                                   38.3%;
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34.8%;
                      1987
                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                  -EERMKEED 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 147; DB 2;
Pred. No. 2.6e-05;
17; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
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cottonseed
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embryogenesis and
                                                                                                                                                                                                                                                                                                                                                                                                   14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                               30-Sep-1993
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germination.
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R:Yamada, K.; Shimada, T.; Kondo, M.; Nishimura, M.; Hara-Nishimura, J. Biol. Chem. 274, 2563-2570, 1999
A;Title: Multiple functional proteins are produced by cleaving Asn-G: A;Reference number: 222767; MUID:99107919
A;Accession: T44430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: glycinin
F;1-24/Domain: signal sequence #status
F;25-605/Product: alpha-globulin type F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Status: not compared with conceptual translation A:Molecule type: DNA A:Residues: 1-605 <CHL>
A; Residues: 1-810 < YAM>
                 A; Molecule type: mRNA
                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                   C; Accession: T44430
                                                                                                                                                                                    protein PV100 [imported] - winter squash
C;Species: Cucurbita maxima (winter squash)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                        T44430
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A; Mobile element:
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A;Cross-references: EMBL:AF000580; NID:g3068582; PIDN:AAC14390.1;
A;Experimental source: strain WS2162
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: Z14684; MUID:98198836
A;Accession: T02634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Rieben Jr., W.K.; Gonzales, C.M.; Gonzales, S.T.; Pilkington, K.J.; Kiyosawa, H.; H
Genetics 148, 1117-1125, 1998
A;Title: Dictyostelium discoideum nuclear plasmid Ddp5 is a chimera related to the Dd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rep protein homolog - slime mold (Dictyostelium discoideum) plasmid Ddp5 C;Species: Dictyostelium discoideum C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 29-Oct-1999 C;Accession: T02634
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                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 QRDPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQ-QREDEEKYE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQQCVKECREQYQEDPWKGERENKWREEEEEESD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPQRRYQDCRQHCQQEERRLRPHCEQSCREQYEKQQQQQPDKQFKECQQRCQWQEQRPER 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 116.5; DB Pred. No. 0.014;
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Pred. No. 0.00067;
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                                                                                                      Asn-Gln bonds
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A;Cross-references: EMBL:AB019195; NID:g3808061; PIDN:BAA34056.1; PID:g3808062

sin

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hypothetical protein 1 - African malaria mosquito (fragment)
C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 17-Apr-1993 **sequence_revision 17-Apr-1993 **text_change 09-Sep-1997
C;Accession: $27770
R;Besansky, N.J.; Paskewitz, S.M.; Mills-Hamm, D.M.; Collins, F.H.
submitted to the EMBL Data Library, June 1992
A,Description: Distinct families of site-specific retroposons occupy identic A;Reference number: $27770
A;Accession: $27770
A;Accession: $27770
A;Accession: $27770
A;Residues: 1-613 <BES>
A;Cross-references: EMBL:M93690; NID:g159615; PID:g159616
                                                                                                                                                                                                                                               A:Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Rosidues: 1-1737 <GEI>A:Cross-references: GB:AFE090533; NID:g5714395; PIDN:AAD47903.1; PID:g5714396 A;Experimental source: Strain AX2
                                                                                                                                                                                                                                                                                                                                                                                                          R;Geissler, H.; Schwarz, E.C.; Soldati, T. submitted to GenBank, September 1998
A;Description: Identification of two novel and highly divergent myosins in Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unconventional myosin heavy chain MyoM - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Species: Dictyostelium discoideum
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 08-Sep-2000
C:Accession: A59235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
A59235
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                                                                                                                                                                 C; Superfamily: myosin motor domain homology F:62-874/Domain: myosin motor domain homology #status atypical
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A; Accession: A59235
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Best Local S
Matches 25
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les 18; Conser
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NRORDPOOQYEOCOKHCORRETEPRHMQTCQORCERRYEKE-KRKQQKRYEEQQREDEEK 59
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                                                               27.3%; Solution 27.3%; Solution 27.3%; P. 25; Conservative 20;
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                                                             Score 105; DB 2
Pred. No. 0.19;
20; Mismatches
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                                                                                                       Length 1737;
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trfA protein - slime mold (Dictyostelium discoideum)
C; Species: Dictyostelium discoideum
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_ch
C; Accession: T14004
R; Saito, J.; Adachi, H.; Sutoh, K.
J. Biol. Chem. 273, 24654-24659, 1998
A; Title: Dictyostelium TRFA homologous to yeast Ssn6 is req
A; Reference number: Z17852; MUID:98406112
A; Accession: T14004
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1390 <SAID
A; Residues: 1
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A;Map position: X
A;Introns: 12/1; 106/3;
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A;Accession: T19201
A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-385 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AB009080; NID:d1228566; PID:d1034109; PIDN:BAA33143.1
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                                                                                                                                                                                               Query Match 27.1%;
Best Local Similarity 23.9%;
Matches 16; Conservative 3
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Best Local
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                                                              Local Similarity
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ERMKEED 68
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27.6%;
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                                                                                                                                                                                               Score 104; DB Pred. No. 0.19; 0; Mismatches
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151 QQQQQQD

157

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J. Biol. Chem. 268, 12164-12176, 1993
A;Title: The structure of human trichohyalin. Potential multiple roles as a function d.Reference number: A45973; MUID:93280194
A;MoLecule ****Construction of the construction of the constr
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R;Fietz, M.J.; Rogers, G.E.
submitted to the EMBL Data Library, December 1992
submitted to the EMBL Data Library, December 1992
submitted to the EMBL Data Library, December 1992
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                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: trichohyalin; calmodulin repeat homology C;Keywords: calcium binding; citrulline; EF hand; hair; F;49-81/Domain: calmodulin repeat homology <EF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-1407 <FIE>
A;Residues: 1-1407 <FIE>
A;Cross-references: EMBL:219092; NID:91746; PIDN:CAA79519.1; PID:91747
C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root Covalent modifications to this protein include conversion of arginine to citrulline an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 12-Mar-1993 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999
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C;Superfamily: trichchyalin; calmodulin repeat homology
C;Keywords: calcium binding; citrulline; EF hand; hair; tandem repeat
F;49-81/Domain: calmodulin repeat homology <EF2>
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A;Residues: 1-1898 <-LEE>
A;Residues: 1-1898 <-LEE>
A;Cross-references: GB:LO9190; NID:g292835; PIDN:AAA65582.1; PID:g292836
A;Note: authors translated the codon AGG for residue 1714 as Pro
C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root sh
Covalent modifications to this protein include conversion of arginine to citrulline and
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C;Date: 03-May-1994 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999
C;Date: 03-May-1994 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999
C;Accession: A45973
R;Lee, S.C.; Kim, I.G.; Marekov, L.N.; O'Keefe, E.J.; Parry, D.A.D.; Steine:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 46/3
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Best Local Similarity
Matches 25; Conser
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                                                                                                                                                                                                     Local Similarity
nes 25; Conserv
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                                                                                                      QRDPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQK------RYEEQQR 54
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      83
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                                                                                                                                                                                                  Score 102; DB 1;
Pred. No. 0.28;
0; Mismatches 19
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Pred. No. 0.26;
9; Mismatches
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C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17218
                                                                C; Accession: T30989
                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change
                                                                                                                                                            serine/threonine protein kinase NIK - mouse N; Alternate names: Nck interacting kinase
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A; Residues: 1-1027 <AAA>
A; Cross-references: EMBL:AL137755
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C; Date: 04-Feb-2000 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein DKF2p434A025.1 - human (fragment) C;Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: DKFZp434P1750.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: adult testis; clone DKFZp434P1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Molecule type: mRNA
A;Residues: 1-233 <POU>
A;Cross-references: EMBL:AL117408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z18723
A; Accession: T17218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein DKFZp434P1750.1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вр
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
Y.C.; Han, J.; Xu, S.;
J. 16, 1279-1290, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 RQKRIEQQKEQRRRLEEQQRREEREARRQQEREQR---RREQEEKRRLEELERRRKEEEEERR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 KETRKQEKERQKQEKERQKQEKEREKERQKQEKEREKQEKERQKQE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 EQEERREQRIEQEE 327
                                                                                                                                                                                                                                                                                                                                                                      192 RAEEEKRRVEREQEYIRRQLEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 KHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 35.8 nes: 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   55 -----EDEEKYEERMKEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RQRDPQQQYEQCQK--HCQRRETEPRHMQTCQQRCERRYEKEKRK----QQKRYEEQQR- 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.3%;
36.1%;
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                                  Cobb, M.; Skolnik, E.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 101; DB:
Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 101; DB:
Pred. No. 0.08;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   89
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